



OIKE

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/896,186B

TIME: 11:54:48

Input Set : A:\31814A Sequence Listing.txt

Output Set: N:\CRF3\04162002\I896186B.raw

p.6

ENTERED

3 <110> APPLICANT: Joshua Z. Levin
 4 Ken Phillips
 5 Greg Budziszewski
 6 Fred Meins
 7 Zhenya Glazov
 9 <120> TITLE OF INVENTION: Methods of Controlling Gene Expression
 11 <130> FILE REFERENCE: PB/5-31481A
 W--> 12 <140> CURRENT APPLICATION NUMBER: 09/896,186B
 C--> 13 <141> CURRENT FILING DATE: 2002-04-04
 15 <160> NUMBER OF SEQ ID NOS: 38
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 942
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Arabidopsis thaliana
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 27 accgtacaag ctacaacctc cgtccatggc cagaggagg atccaaatca aatccccaat 180
 28 aatatccgtc gccaatggc tcgttccatc acttcttcta catcttataa acgatttcct 240
 29 ctctcccggt gccgagctag gaattttcca gcaatgaggt ttggtggtag gattttgtat 300
 30 agcaagactg ctactgaggt tgataagcga gcaatgcagc ttattaaagt tcttgatacc 360
 31 aagagagatg aatctggaat agcttttgtt ggcttgata ttgagtggag accaagtttt 420
 32 agaaaagggt ttctcccggt gaagggtgcg actgtccaga tatgtgtaga tagtaattat 480
 33 tgtgatgtta tgcataattt tcattctggt atccctcaaa gtctccaaca tcttattgaa 540
 34 gattcaacac ttgtaaagg aggtattgga attgatggtg actctgtgaa gcttttccat 600
 35 gactatggag ttagtatcaa agatgttgag gatctttcag atttagccaa ccaaaaaatt 660
 36 ggtggagata aaaaatgggt ccttgccctc ctaactgaga cacttgtttg caaagagctc 720
 37 ctgaagccaa acagaatcag gcttggaac tgggagttt atcctctgtc aaagcagcag 780
 38 ttacaatacg cagcaacgga tgcttatgct tcatggcatc ttacaagggt aacaacaacg 840
 39 aaaaaccatc ttctcacact caacgacctt gaagcaaaaa tctcacatcg ttctaattat 900
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 44 <211> LENGTH: 313
 45 <212> TYPE: PRT
 46 <213> ORGANISM: Arabidopsis thaliana
 48 <400> SEQUENCE: 2
 49 Met Ser Ser Ser Asn Trp Ile Asp Asp Ala Phe Thr Glu Glu Glu Leu
 50 1 5 10 15
 52 Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser
 53 20 25 30
 55 Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val
 56 35 40 45

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58 His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
59      50                      55                      60
61 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
62 65                      70                      75                      80
64 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
65                      85                      90                      95
67 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
68                      100                      105                      110
70 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
71                      115                      120                      125
73 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
74                      130                      135                      140
76 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
77 145                      150                      155                      160
79 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
80                      165                      170                      175
82 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
83                      180                      185                      190
85 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
86                      195                      200                      205
88 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
89                      210                      215                      220
91 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
92 225                      230                      235                      240
94 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
95                      245                      250                      255
97 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
98                      260                      265                      270
100 His Leu Tyr Lys Val Thr Thr Thr Lys Asn His Leu Leu Thr Leu Asn
101                      275                      280                      285
103 Asp Leu Glu Ala Lys Ile Ser His Arg Ser Asn Tyr Asn Thr Val Thr
104                      290                      295                      300
106 Cys Arg Lys Pro Gly Gly Tyr Leu Arg
107 305                      310
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111 <211> LENGTH: 1929
112 <212> TYPE: DNA
113 <213> ORGANISM: Arabidopsis thaliana
115 <400> SEQUENCE: 3
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117 aagaaggtaa tcgatgtgaa agtggctgag agtgataagg gattcgcgaa atttggcaag 120
118 gcagaggttc cgtttcatat accgacgtta acgaagcctc aagaggagta taagattttg 180
119 gtagacaatg ctaataatcc ttttgagcat gttttgttgg agaagagtga agacggtctt 240
120 cggttcattc atccactgga ggaactatct gtgatggact ttgttgatag aaatctaagt 300
121 gagatgagac ctgttaagcc tctccattg gaagagactc cattcaagct agttgaagaa 360
122 gtcaaagatc ttgaggactt agctgctgca ttgcaaagtg ttgaagagtt tgctgtcgat 420
123 ctggagcata atcagtatag aacttttcaa ggattaacat gcttgatgca aatctctact 480
124 agaaccgagg attatattgt tgatatattc aagctttggg atcacattgg tccttatcta 540
125 agggaaactct tcaaagaccc taaaaagaaa aaggtaatcc atggagcaga tcgagatatt 600

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126 atttggcttc aacgggactt tggcatttat gtctgcaatc tttttgacac aggacaggct 660
127 tcaaggggtgc taaagctgga gagaaatagt ctggaatttc ttctgaagca ttattgtgga 720
128 gttgctgcaa acaaagaata ccaaaaagca gactggagaa taagaccctt tccagatgta 780
129 atgaaaagat atgctagaga agatacacat tatcttttgt acatttatga tgtaatgcga 840
130 atggagttgc acacaatggc aaaggaagat gagcaatctg actctcctct ggtagagggtg 900
131 tacaagcgca gttatgacgt gtgcatgcaa ctatatgaaa aagagctttg gactagggat 960
132 tcatactctc acgtttatgg ggttcagaca ggtaatctca atgcggttca actttccatt 1020
133 gttgcgctgc aggggctttg tgaatggcgg gatcggattg cacgcgcaga tgatgagagc 1080
134 accggttatg tattgccaaa taaaactctt tttgacatag ccaaggagat gccaattggt 1140
135 gttgcccagt tgcgccgttt gttgaagtca aagcttcctt acctcgagcg taattttgac 1200
136 gcagtgatca gtgtcatcag acgatcaatg caaaatgcag cggcattcga gccagttggt 1260
137 caatctttga aagataggcg tctgaaaca gtggttgaaa tgaatataga acctaaagatt 1320
138 gagaaaacag acacaggagc ttcagcgtct tctctgagtc tggagaaggt ttgtgtggat 1380
139 gattcaaaga aacaaagcag tggttttgga gttttgccgt taaagaggaa gttggaaagt 1440
140 gacaaaacgg tggttgaaaa gaatatcgaa cctaagattg agaaaacagg cacagaagct 1500
141 tcagcttctt ctctgagttc gaagaaggtt tgtgtggatg attcaaagaa acaaagcagt 1560
142 ggttttgag tttgtctgtc aaagaggaag tttgaaagtg ataacaagaa gttgcaggta 1620
143 aaagaagagg tcaaagtgtc caagtccaag ccagataagg taatcatagt ggtggatgat 1680
144 gatgatgatg atgatgatga tgagtcttat gaacagagca cgaaagccgc tgatgctttg 1740
145 gacagagttt cggaaacgcc ttcgaaggga tcaccatcgt tgactcaaaa gccgaagaca 1800
146 tgtaatacag aggttattgt gttagacgat gatgatgact cggaaagcag agaagatgaa 1860
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148 aacatttag                                     1929

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151 <210> SEQ ID NO: 4

152 <211> LENGTH: 642

153 <212> TYPE: PRT

154 <213> ORGANISM: Arabidopsis thaliana

156 <400> SEQUENCE: 4

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161           20           25           30
163 Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
164           35           40           45
166 Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
167           50           55           60
169 Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
170  65           70           75           80
172 Arg Phe Ile His Pro Leu Glu Glu Leu Ser Val Met Asp Phe Val Asp
173           85           90           95
175 Arg Asn Leu Ser Glu Met Arg Pro Val Lys Pro Leu Pro Leu Glu Glu
176           100          105          110
178 Thr Pro Phe Lys Leu Val Glu Glu Val Lys Asp Leu Glu Asp Leu Ala
179           115          120          125
181 Ala Ala Leu Gln Ser Val Glu Glu Phe Ala Val Asp Leu Glu His Asn
182           130          135          140
184 Gln Tyr Arg Thr Phe Gln Gly Leu Thr Cys Leu Met Gln Ile Ser Thr
185 145           150           155           160
187 Arg Thr Glu Asp Tyr Ile Val Asp Ile Phe Lys Leu Trp Asp His Ile

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188          165          170          175
190 Gly Pro Tyr Leu Arg Glu Leu Phe Lys Asp Pro Lys Lys Lys Lys Val
191          180          185          190
193 Ile His Gly Ala Asp Arg Asp Ile Ile Trp Leu Gln Arg Asp Phe Gly
194          195          200          205
196 Ile Tyr Val Cys Asn Leu Phe Asp Thr Gly Gln Ala Ser Arg Val Leu
197          210          215          220
199 Lys Leu Glu Arg Asn Ser Leu Glu Phe Leu Leu Lys His Tyr Cys Gly
200 225          230          235          240
202 Val Ala Ala Asn Lys Glu Tyr Gln Lys Ala Asp Trp Arg Ile Arg Pro
203          245          250          255
205 Leu Pro Asp Val Met Lys Arg Tyr Ala Arg Glu Asp Thr His Tyr Leu
206          260          265          270
208 Leu Tyr Ile Tyr Asp Val Met Arg Met Glu Leu His Thr Met Ala Lys
209          275          280          285
211 Glu Asp Glu Gln Ser Asp Ser Pro Leu Val Glu Val Tyr Lys Arg Ser
212          290          295          300
214 Tyr Asp Val Cys Met Gln Leu Tyr Glu Lys Glu Leu Trp Thr Arg Asp
215 305          310          315          320
217 Ser Tyr Leu His Val Tyr Gly Val Gln Thr Gly Asn Leu Asn Ala Val
218          325          330          335
220 Gln Leu Ser Ile Val Ala Leu Gln Gly Leu Cys Glu Trp Arg Asp Arg
221          340          345          350
223 Ile Ala Arg Ala Asp Asp Glu Ser Thr Gly Tyr Val Leu Pro Asn Lys
224          355          360          365
226 Thr Leu Phe Asp Ile Ala Lys Glu Met Pro Ile Val Val Ala Gln Leu
227          370          375          380
229 Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
230 385          390          395          400
232 Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
233          405          410          415
235 Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
236          420          425          430
238 Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
239          435          440          445
241 Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
242          450          455          460
244 Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
245 465          470          475          480
247 Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
248          485          490          495
250 Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
251          500          505          510
253 Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
254          515          520          525
256 Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
257          530          535          540
259 Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
260 545          550          555          560

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262 Asp Asp Asp Asp Asp Asp Asp Glu Ser Tyr Glu Gln Ser Thr Lys Ala
263                               565                               570                               575
265 Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
266                               580                               585                               590
268 Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
269                               595                               600                               605
271 Asp Asp Asp Asp Asp Ser Glu Ser Arg Glu Asp Glu Asp Met Arg Arg
272                               610                               615                               620
274 Arg Ser Glu Lys His Arg Arg Phe Met Asn Met Lys Arg Gly Phe Leu
275 625                               630                               635                               640
277 Asn Ile
281 <210> SEQ ID NO: 5
282 <211> LENGTH: 714
283 <212> TYPE: DNA
284 <213> ORGANISM: Arabidopsis thaliana
286 <400> SEQUENCE: 5
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289 ggatttttga gaggagagtg ttcattggaa atgagtgatt catatgtgtg ggttgagaca 180
290 gagtcgcagt taaaggaact tgcagaaata ttagcaaaaag aacaagtttt tgcgggttgac 240
291 actgagcagc atagttttgcg gtcgttttctt ggttttactg ctctaattca gattttctaca 300
292 catgaggaag acttttttggg ggacacaatt gcgttacatg atgtaatgag tattcttcgt 360
293 cctgttttct ctgatcctaa tatttgtaag gtgtttcacg gggctgacaa cgatgttatc 420
294 tggcttcaaa gagacttcca tataatatgtt gttaatatgt ttgatactgc caaggcatgt 480
295 gaagtgttgt caaagcctca acgatcactg gcatacttac ttgagacagt atgtggagtg 540
296 gctactaaca aattgctgca gcgtgaagat tggagacagc gtcctctgtc cgaagagatg 600
297 gtgcgatatg ctagaacaga tgcacactat ctgctttata ttgcagatag tttgacaact 660
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302 <211> LENGTH: 237
303 <212> TYPE: PRT
304 <213> ORGANISM: Arabidopsis thaliana
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310 Glu Lys Pro Ser Asn Gly His Pro Tyr Glu Thr Glu Ile Thr Val Leu
311 20 25 30
313 Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
314 35 40 45
316 Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
317 50 55 60
319 Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
320 65 70 75 80
322 Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
323 85 90 95
325 Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
326 100 105 110
328 His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
329 115 120 125

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/16/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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